FIGURE 1

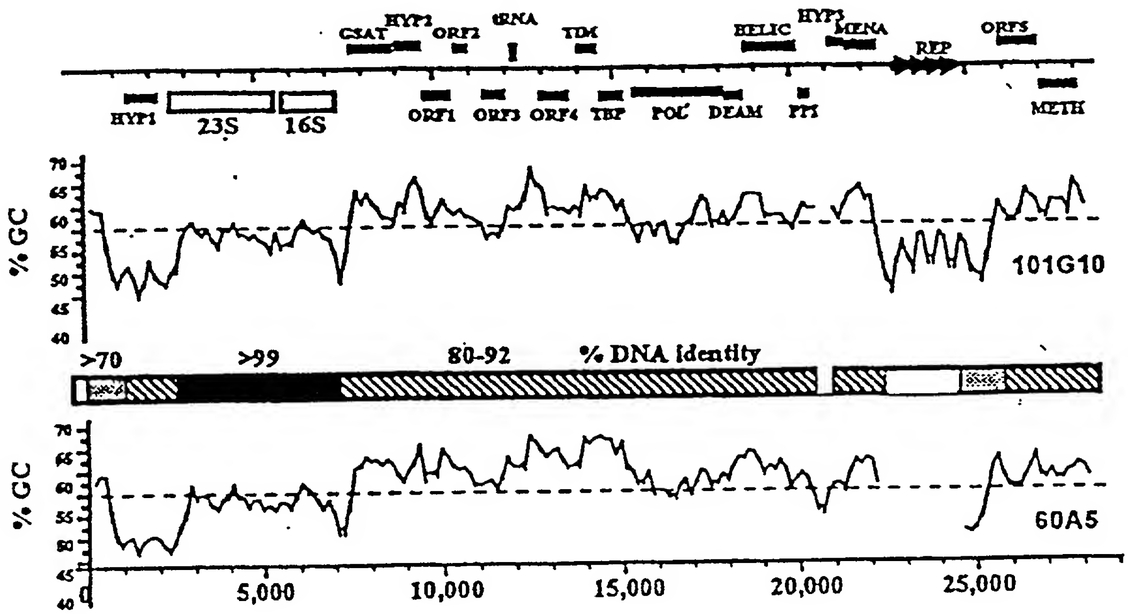

Figure 2

SQ. ID. NO.	Gene	Strain	TATA Box	Coding Start	TATA to Start (bp)
81	Hypoth 03	A	AAGCTAGACT TTTAAT TGGG ATCCGGCGGG	GCGGCGCATG ~~~~~~~~~~ ~~~~~~~~~~	25
82		B	AAGCTAAACT TTTAAT TGGG ATCCGGCGAG	CCGGCGCGTG ~~~~~~~~~~ ~~~~~~~~~~	
83	Hypoth 02	A	GGAAACTTTG ATTATA CGGG CGTGCTGCCC	CGGGGCCCAT G~~~~~~~~~ ~~~~~~~~~~	26
84		B	GGAAACTTTG ATTATA CGGG CGTACATTCC	CGGGGCCCAT G~~~~~~~~~ ~~~~~~~~~~	
85	ORF 02	A	AAGGCAAGGT AATAAT AGCC TGCCGTCTGT	AACGGCCGTA TG~~~~~~~~ ~~~~~~~~~~	27
86		B	ACGGCAAGGT AATAAT AGCC TGCCGTCCGT	ACCTGCCGTA TG~~~~~~~~ ~~~~~~~~~~	
87	ORF 03	A	CATGGAACTA GATATT AACC GGTTCCGCGG	ATCCCATGCA TG~~~~~~~~ ~~~~~~~~~~	27
88		B	CATGGAACTA GATAAT AACC GGTCCCGCGG	GTACAATGCA TG~~~~~~~~ ~~~~~~~~~~	
89	PPI	A	ATACCGAGAA GTTATA GCAG GGTATGGAAT	GTGCGCGCGC ATG~~~~~~~ ~~~~~~~~~~	28
90		B	AGCACGACAA GTTATA GCAG GGTACAAAGG	AGCAGCGCAC ATG~~~~~~~ ~~~~~~~~~~	
91	GSAT	A	ATCCGCCCTG ATTAAA TTAT GGGGGGAGCG	GCCTGCTGCC GTG~~~~~~~ ~~~~~~~~~~	28
92		B	ATCCGGCCTC ATTAAA TTAC GGGGGGTACA	ACCTGCTGCC GTG~~~~~~~ ~~~~~~~~~~	
93	ORF 05	A	CCTTCATACA CATAAA TCCC GCTTGGATGT	GCGGCTGCGC ATG~~~~~~~ ~~~~~~~~~~	28
94		B	ACTTCATACA CATAAA TCCC GCCTGAACGG	TCGTCCGCGC ATG~~~~~~~ ~~~~~~~~~~	
95	deaminase	A	.GGCATATAC CATAAT ATGC CGGGCGGTGG	CACCATGGCC GTTG~~~~~~ ~~~~~~~~~~	29
96		B	CCGCATATAC CATAAT ATGC CGGGCGGGGG	CAGGCTGCCC .GTG~~~~~~ ~~~~~~~~~~	
97	RNA helic	A	TGTACGAAAC CATAAA ACAA CAGGCCGCGT	CAGGGCCGCG CGTG~~~~~~ ~~~~~~~~~~	29
98		B	GGGTAGAAAC CATAAA ACAA CAGGCCGCGG	CAGGGCG.CG CGTG~~~~~~ ~~~~~~~~~~	
99	ORF 06	A	..ACACGCAG TATAAA CGGG GGCCCGGGCG	GCGCGTATCA CATG~~~~~~ ~~~~~~~~~~	29
100		B	ATACACGTGG TATAAA CAGA GG.CCGGACG	GCGCGGACCA CATG~~~~~~ ~~~~~~~~~~	
101	tRNA-tyr	A	GCGATAGTTA TTTAAA ACTA GGATGCCGAT	CACGGATCGT CCCA~~~~~~ ~~~~~~~~~~	29
102		B	GCGATAGTTA TTTAAA ACTA GGATGCCGGG	CACCCGTCGT CCCA~~~~~~ ~~~~~~~~~~	
103	TBP	A	CCGGGCCCCG GTTAAA ATAG CG.CACGGGC	GGATCCTGAC CAATG~~~~~ ~~~~~~~~~~	30
104		B	CCGGGCCCCG GTTAAA ATAG AGTGCGGCCG	GGCACCGGAT CAATG~~~~~ ~~~~~~~~~~	
105	TIM	A	GCGTCGATAG AATAAA TACG CGCAGGGGGC	CCCGTGGCGC GATCGCCCGT G~~~~~~~~~	36
106		B	GCGTCGATAG AATAAA TACG CGC.GGGGCC	GCGGTGC... GATCGCCCGT G~~~~~~~~~	
107	Hypoth 01	A	ATTTCAACTA CATAAA TGCC TAGTTACGCA	GAAATAGCAA ACGACGTACT TCGACTAATG	45
108		B	ACTTCAACTA CATAAA TGCC TAGCTACGCA	GAAATATCAA ACAAAGTACT TCGACTAATG	
109	ORF 01	A	ACGGCAGGCT ATTATT ACCT TGCCTTGCGT	TGTA //..G CGGGGTGCGG CAGGGGATG	52
110		B	ACGGCAGGCT ATTATT ACCT TGCCGTGTG.	TACA //..G AGGGGGCCTG CCGGGAGTG	
111	Methylase	A	CTACAACGAT TTTAAG TCGG CGCCGGGGCA	GCCG.//..G ATGTGGGGCA GGCAACATG	104
112		B	CTACAAAGAT TTTAAG ACGG CGCGGGTGCC	GCGG.//..T GGCACGGGGG CCTATCTTG	
113	16S RNA	A	TCGGCGATGG TTTATA TGCC CATGGACGGG	CCGATCCGAT CGTACGTGAC GC.//..AAT	220
114		B	CCGGCGATGG TTTATA TGCC CATGGACAAG	GCGATCCGAT CGTACGTGAC GC.//..AAT	
	Archaeal promoter consensus		YTTAWA		

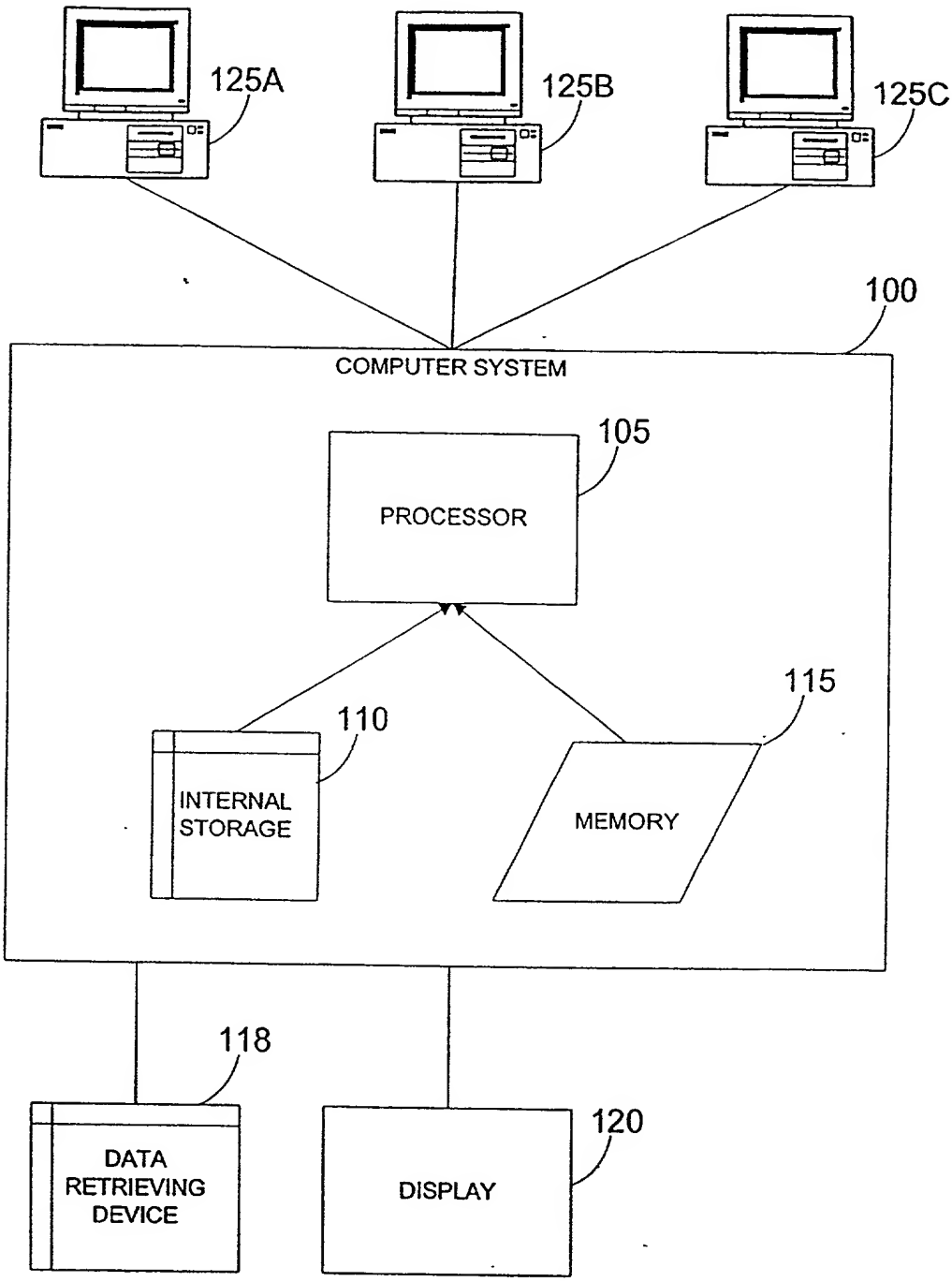
125A
125B
125C
100
COMPUTER SYSTEM
105
PROCESSOR
110
INTERNAL STORAGE
115
MEMORY
118
DATA RETRIEVING DEVICE
120
DISPLAY

FIGURE 3

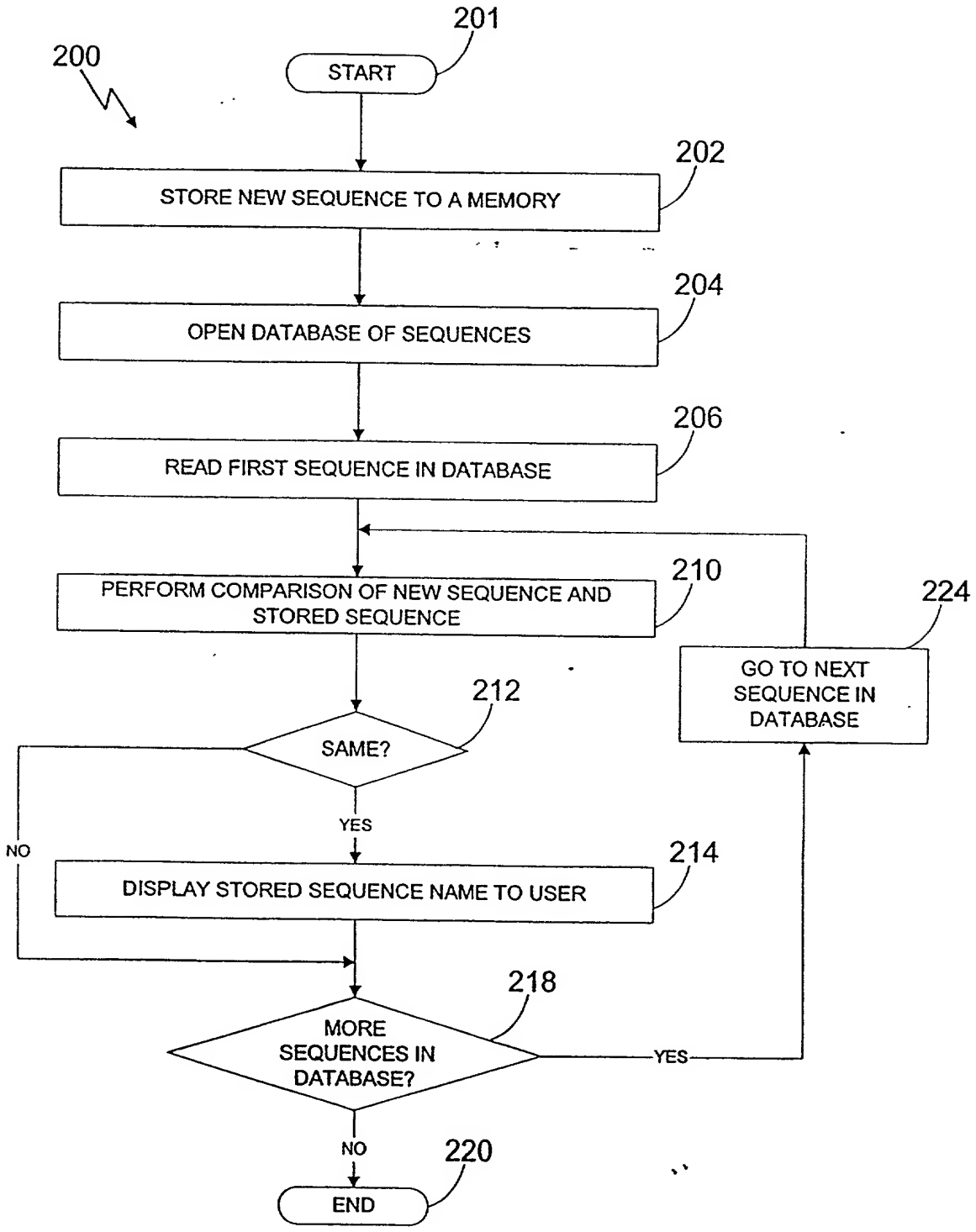
200
201
START
202
STORE NEW SEQUENCE TO A MEMORY
204
OPEN DATABASE OF SEQUENCES
206
READ FIRST SEQUENCE IN DATABASE
210
PERFORM COMPARISON OF NEW SEQUENCE AND STORED SEQUENCE
212
SAME?
YES
NO
214
DISPLAY STORED SEQUENCE NAME TO USER
218
MORE SEQUENCES IN DATABASE?
YES
NO
220
END
224
GO TO NEXT SEQUENCE IN DATABASE

FIGURE 4

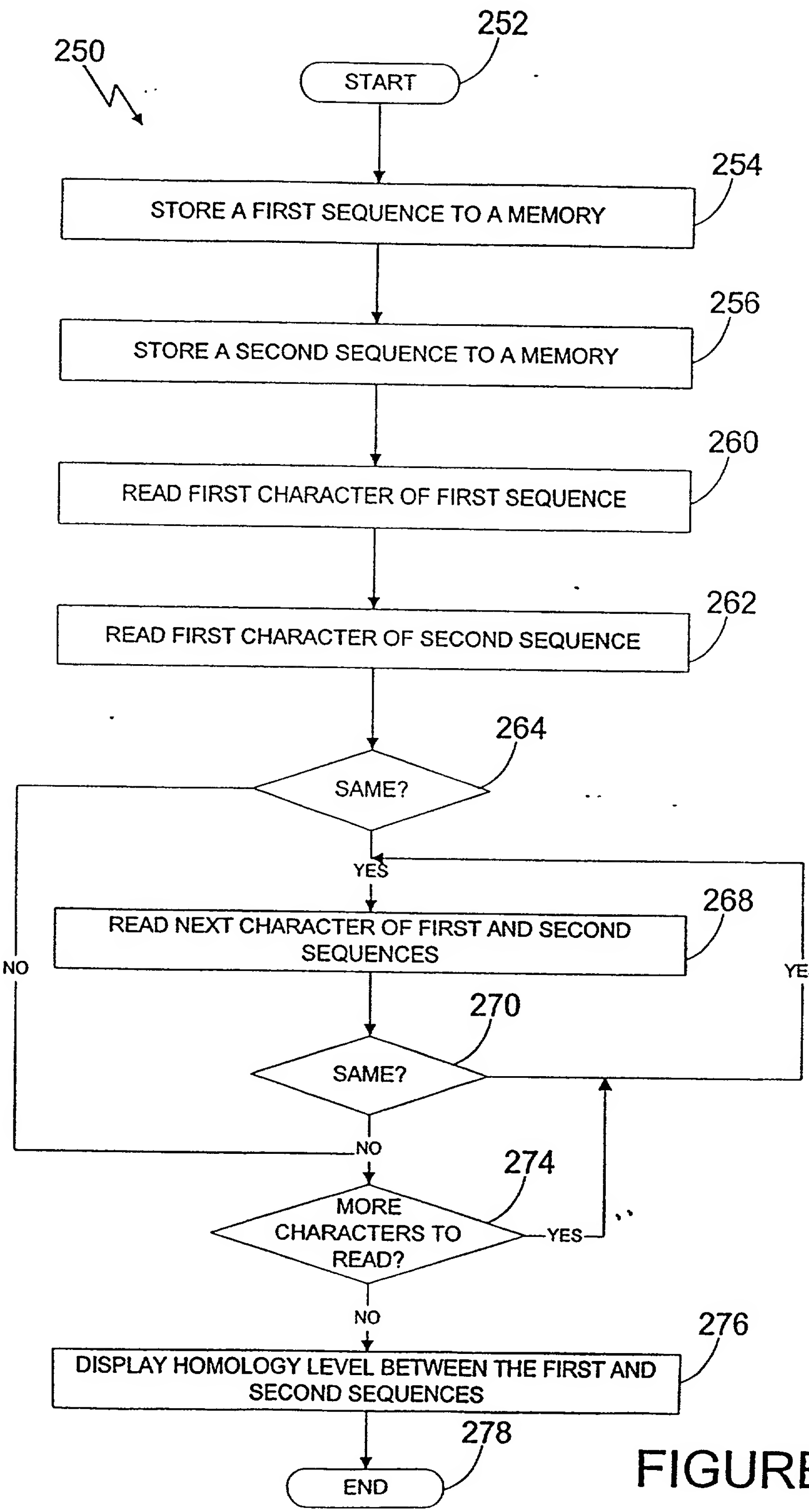

FIGURE 5

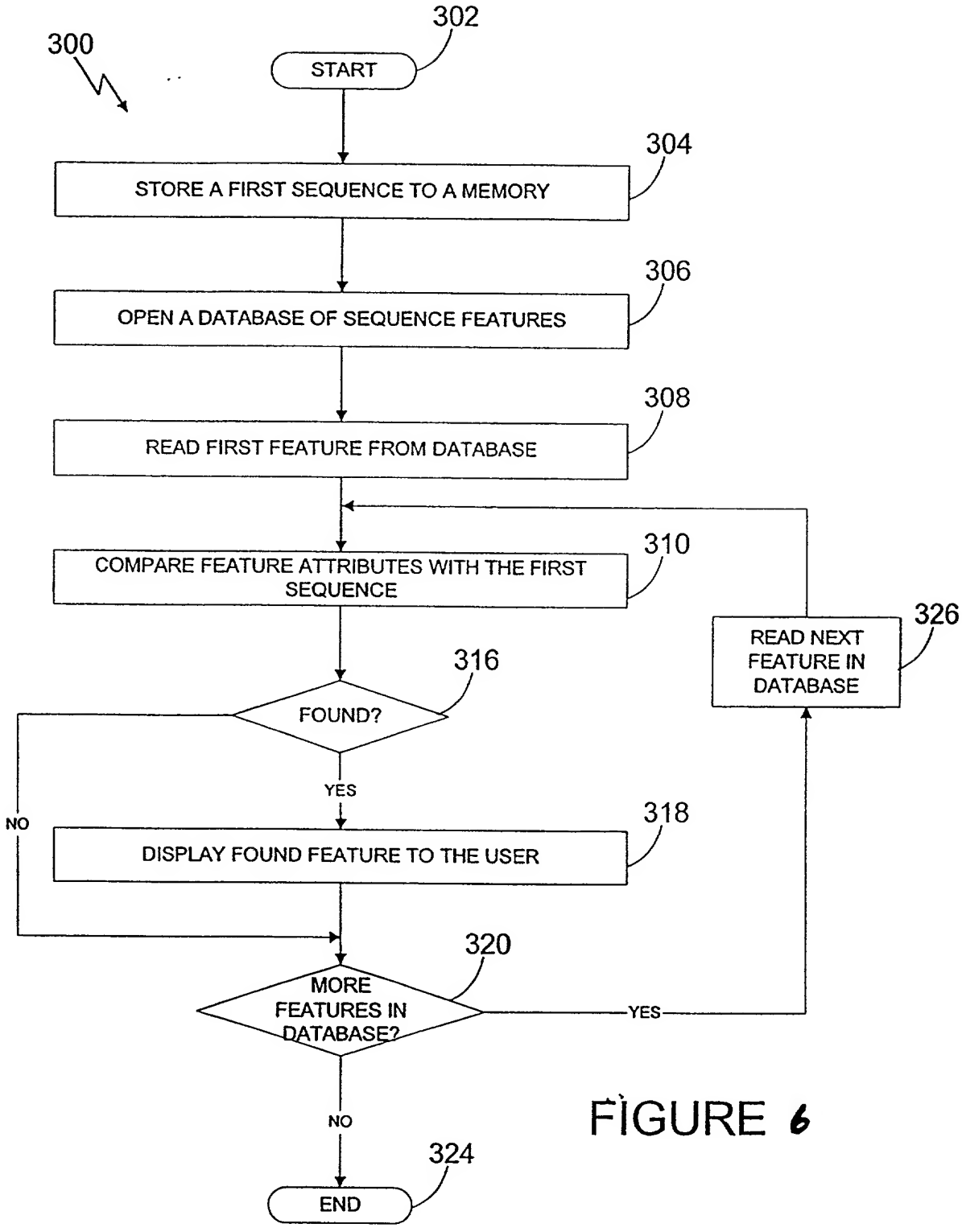
300
302
START
304
STORE A FIRST SEQUENCE TO A MEMORY
306
OPEN A DATABASE OF SEQUENCE FEATURES
308
READ FIRST FEATURE FROM DATABASE
310
COMPARE FEATURE ATTRIBUTES WITH THE FIRST SEQUENCE
316
FOUND?
YES
NO
318
DISPLAY FOUND FEATURE TO THE USER
320
MORE FEATURES IN DATABASE?
YES
NO
324
END
326
READ NEXT FEATURE IN DATABASE

FIGURE 6